

#8



032301.195.seq.ST25.txt
SEQUENCE LISTING

<110> MOCKEL Bettina et al.

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE cstA GENE

<130> 032301 WD 195

<160> 7

<170> PatentIn version 3.1

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<211> 2718

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (200)..(2515)

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tggccgaact ttcctttttc tgcattgcatt tctgcacaca gtttctgccc gctgtttctg 1
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cccgtgtgtt ctacgcata gtg gct ttg aaa cga ccc gaa gag aaa aca gta 2
32

Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val

1 5 10

aag atc gtg acc ata aaa cag act gac aac atc aat gac gat gat ttg 2
80

Lys Ile Val Thr Ile Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu

15 20 25

gtg tac agc aac gct act gac ctt cca gta ggc gtg aag aag tcc cct 3

032301.195.seq.ST25.txt

28

Val Tyr Ser Asn Ala Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro

30

35

40

aaa atg tca ccg acc gcc cgc gtt ggt ctc ctt gtc ttt ggg gtt atc 3

76

Lys Met Ser Pro Thr Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile

45

50

55

gcg gcg gtg ggt tgg gga gca atc gct ttc tcc cgt ggc gaa aca atc 4

24

Ala Ala Val Gly Trp Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile

60

65

70

75

aac tct gtg tgg ctg gtt ttg gcg gca gtt ggt tcc tat atc att gcg 4

72

Asn Ser Val Trp Leu Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala

80

85

90

ttt tct ttc tat gcc cga ctg att gaa tac aaa gtt gtt aag ccg aaa 5

20

Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys

95

100

105

gat cag cga gca acc ccg gcg gaa tac gtt aat gac ggc aag gac tat 5

68

Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr

110

115

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gtc cca acg gat cgt cgt gtg ctt ttt ggc cac cac ttt gca gct att 6

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Val Pro Thr Asp Arg Arg Val Leu Phe Gly His His Phe Ala Ala Ile

125

130

135

gca ggt gcc ggt cca ttg gtt gga cct gtc atg gcc gcg cag atg ggc 6
64

140 145 150 155

tac ctg cca ggc acc ttg tgg att atc ctc ggt gtg att ttc gcc ggt 7
12

160 165 170

gca gtg cag gac tac cta gtg ctg tgg gtg tct act cgt agg cgt gga 7
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175 180 185

cgc tca ctt ggc cag atg gtt cgt gat gaa atg ggc acg gtc ggt gga 8
08

190 195 200

gct gcc ggt atc ttg gcg acc atc tcc atc atg atc atc att atc gcg 8
56

205 210 215

gtg ctc gca ttg atc gtg gtt aat gca ctg gct gat tca cca tgg ggc 9
04

220 225 230 235

gtt ttc tcc atc acc atg acc atc cca att gca ctg ttc atg ggt gtg 9
52

240 245 250

032301.195.seq.ST25.txt

tac ttg cgt tac ctg cgc cca ggt cgt gtt act gaa gtg tcc atc atc 10
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Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile

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ggt gtg gca ctg ctc ctg ctg gct atc gtt gct ggt ggt tgg gtt gca 10
48

Gly Val Ala Leu Leu Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala

270

275

280

gac acc tca tgg ggc gtg gaa tgg ttc acc tgg tct aag acc act ttg 10
96

Asp Thr Ser Trp Gly Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu

285

290

295

gcg ttg gcc ttg atc ggt tac gga atc atg gct gcg att ttg ccg gtg 11
44

Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val

300

305

310

315

tgg ctg ctg ctt gca ccg cgc gat tac ctg tct acc ttt atg aag atc 11
92

Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile

320

325

330

ggc gtc atc ggt ctg ttg gca gtg ggt att ttg ttc gca cgt cct gag 12
40

Gly Val Ile Gly Leu Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu

335

340

345

gtg cag atg cct tcc gtg acc tcc ttc gca ctt gag ggc aac ggt ccg 12
88

Val Gln Met Pro Ser Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro

350

355

360

032301.195.seq.ST25.txt

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365 370 375	
ggt gca ctg tct ggt ttc cac gca ctg att tct tca gga acc aca cca 84	13
Gly Ala Leu Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro	
380 385 390 395	
aag ctt gtg gag aag gaa tcc cag atg cgc atg ctc ggc tac ggc ggc 32	14
Lys Leu Val Glu Lys Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly	
400 405 410	
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Met Leu Met Glu Ser Phe Val Ala Met Met Ala Leu Ile Thr Ala Val	
415 420 425	
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Ile Leu Asp Arg His Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu	
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act ggt gga gat cca gca acc gca gct gag tgg gtt aac tcc att ggg 76	15
Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly	
445 450 455	
ctg aca ggt gcg gat atc acc ccg gaa cag ctg tcg gaa gct gct gaa 24	16
Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu	

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465

470

475

agt gtc gga gaa tcc act gtt att tcc cgt acc ggt ggc gca cca acc 16
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Ser Val Gly Glu Ser Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr

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485

490

ttg gcg ttc ggt atg tct gaa atc ctc tcc gga ttc atc ggc ggc gct 17
20

Leu Ala Phe Gly Met Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala

495

500

505

gga atg aag gcg ttc tgg tac cac ttc gcc atc atg ttt gag gct ctg 17
68

Gly Met Lys Ala Phe Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu

510

515

520

ttc atc ctc act act gtg gat gca ggt act cgt gtg gct cgc ttt atg 18
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Phe Ile Leu Thr Thr Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met

525

530

535

atg acc gat acc ttg ggc aat gtt cca ggt ctg cgc cgt ttc aag gat 18
64

Met Thr Asp Thr Leu Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp

540

545

550

555

cct tca tgg act gtc ggt aac tgg att tct acc gtg ttt gtg tgt gct 19
12

Pro Ser Trp Thr Val Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala

560

565

570

cta tgg ggt gct att ttg ctc atg ggt gtt acc gat cca ctg ggc ggc 19
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Leu Trp Gly Ala Ile Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly

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580

585

atc aac gtg ctt ttc cca cta ttc ggt atc gct aac cag ctg ctc gcc 20
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Ile Asn Val Leu Phe Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala

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595

600

gct att gca ctt gct ctc gtg ctg gtt gtt gtg gtg aag aag ggc ctg 20
56

Ala Ile Ala Leu Ala Leu Val Leu Val Val Val Val Lys Lys Gly Leu

605

610

615

tac aag tgg gcg tgg att cca gct gtt cct ttg gca tgg gat ctc att 21
04

Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile

620

625

630

635

gtc acg atg act gcg tca tgg cag aag att ttc cac tct gat ccg gct 21
52

Val Thr Met Thr Ala Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala

640

645

650

att ggc tac tgg gct cag aac gcg aac ttc cgc gat gca aag tct caa 22
00

Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln

655

660

665

ggc ctt acc gaa ttt ggt gcc gct aaa tct cct gag gca atc gat gcg 22
48

Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala

670

675

680

gtt atc cga aac acc atg att cag ggc atc ttg tcc atc ctg ttc gcg 22
96

032301.195.seq.ST25.txt

Val Ile Arg Asn Thr Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala

685

690

695

gtg ctc gtc ctc gtt gtt gtc ggc gca gcc att gcg gtg tgc atc aag 23
44

Val Leu Val Leu Val Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys

700

705

710

715

tcc atc agg gct cgt gca gcc gga aca cct ttg gag acc act gaa gag 23
92

Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu

720

725

730

cct gat act gaa tct gag ttc ttc gcc cca act gga ttc ctt gca tct 24
40

Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser

735

740

745

tcc agg gat aag gaa gtc cag gcc atg tgg gac gag cgc tac cca ggc 24
88

Ser Arg Asp Lys Glu Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly

750

755

760

ggt gcg ccc gtg tct tct gga ggg cac taaaacatga tggctcttac 25
35

Gly Ala Pro Val Ser Ser Gly Gly His

765

770

tcatgcactg tggaaaatcc cgcgggcggt gtggtggtat ctactgagc tcatggggga 25
95

cacggcgtat toccaagtatg tgggtgcactt aaagcaccac catccggatg ctccgattcc 26
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ctg
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<213> Corynebacterium glutamicum

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Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
130 135 140

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Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile
210 215 220

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
325 330 335

032301.195.seq.ST25.txt

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
 340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
 355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
 370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
 385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
 405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
 420 425 430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
 435 440 445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
 450 455 460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
 465 470 475 480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
 485 490 495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
 500 505 510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
 515 520 525

032301.195.seq.ST25.txt

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
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Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
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Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
 565 570 575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
 580 585 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
 595 600 605

Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
 610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
 625 630 635 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
 645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
 660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
 675 680 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
 690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
 705 710 715 720

032301.195.seq.ST25.txt

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
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Ser Gly Gly His
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ggtatgacta gcccactct aaatgggtgt 1
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20

ggatgacta gccccactct aaatggtgta ggatggtata aatcatctct caatgttact 1
80

tttccattgt taagaattaa caactctcgg tgatttgctg cataccagc tgtcaaagat 2
40

ccgatcatcg gcatacagaa acacccatct ggccgaactt tcctttttct gcatgcattt 3
00

ctgcacacag tttctgcccg ctgtttctgc ccgctgtttc tacgcata gtg gct ttg 3
57

Met Ala Leu

1

aaa cga ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act 4
05

Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr

5

10

15

gac aac atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt 4
53

Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu

20

25

30

35

cca gta ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt 5
01

Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val

40

45

50

ggc ctc ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc 5
49

Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile

55

60

65

gct ttc tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg 5
97

032301.195.seq.ST25.txt

Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala
70 75 80

gca gtt ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att 6
45
Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile
85 90 95

gaa tac aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa 6
93
Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu
100 105 110 115

tac gtt aat gac ggc aag gac tat gtc cca acg gat cgt cgt gtg ctt 7
41
Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu
120 125 130

ttt ggc cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga 7
89
Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly
135 140 145

cct gtc atg gcc gcg cag atg ggc tac ctg cca ggc acc ttg tgg att 8
37
Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile
150 155 160

atc ctc ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg 8
85
Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu
165 170 175

tgg gtg tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt 9

032301.195.seq.ST25.txt

33

Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg

180

185

190

195

gat gaa atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc

81

9

Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile

200

205

210

tcc atc atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat

29

10

Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn

215

220

225

gca ctg gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc

77

10

Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile

230

235

240

cca att gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt

25

11

Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly

245

250

255

cgt gtt act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct

73

11

Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala

260

265

270

275

atc gtt gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg

21

12

Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp

280

285

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032301.195.seq.ST25.txt

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69

Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly

295

300

305

atc atg gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat 13
17

Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp

310

315

320

tac ctg tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg 13
65

Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu Leu Ala Val

325

330

335

ggt att ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc 14
13

Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser Val Thr Ser

340

345

350

355

ttc gca ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca 14
61

Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro

360

365

370

ttc ctg ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca 15
09

Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala

375

380

385

ctg att tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag 15
57

Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln

390

395

400

032301.195.seq.ST25.txt

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405 410 415	
atg atg gca ctg atc acc gct gtt att ctg gat cgt cac ctg tac ttc 53	16
Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His Leu Tyr Phe	
420 425 430 435	
tcc atg aac gct ccg ctg gca ctg act ggt gga gat cca gca acc gca 01	17
Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro Ala Thr Ala	
440 445 450	
gct gag tgg gtt aac tcc att ggg ctg aca ggt gcg gat atc acc ccg 49	17
Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp Ile Thr Pro	
455 460 465	
gaa cag ctg tcg gaa gct gct gaa agt gtc gga gaa tcc act gtt att 97	17
Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser Thr Val Ile	
470 475 480	
tcc cgt acc ggt ggc gca cca acc ttg gcg ttc ggt atg tct gaa atc 45	18
Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met Ser Glu Ile	
485 490 495	
ctc tcc gga ttc atc ggc ggc gct gga atg aag gcg ttc tgg tac cac 93	18
Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe Trp Tyr His	
500 505 510 515	

ttc gcc atc atg ttt gag gct ctg ttc atc ctc act act gtg gat gca 41	19
Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr Val Asp Ala	
520 525 530	
ggt act cgt gtg gct cgc ttt atg atg acc gat acc ttg ggc aat gtt 89	19
Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val	
535 540 545	
cca ggt ctg cgc cgt ttc aag gat cct tca tgg act gtc ggt aac tgg 37	20
Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val Gly Asn Trp	
550 555 560	
att tct acc gtg ttt gtg tgt gct cta tgg ggt gct att ttg ctc atg 85	20
Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile Leu Leu Met	
565 570 575	
ggt gtt acc gat cca ctg ggc ggc atc aac gtg ctt ttc cca cta ttc 33	21
Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe	
580 585 590 595	
ggt atc gct aac cag ctg ctc gcc gct att gca ctt gct ctc gtg ctg 81	21
Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu	
600 605 610	
gtt gtt gtg gtg aag aag ggc ctg tac aag tgg gcg tgg att cca gct 29	22
Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala	

615

620

625

gtt cct ttg gca tgg gat ctc att gtc acg atg act gcg tca tgg cag 22
77

Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala Ser Trp Gln

630

635

640

aag att ttc cac tct gat ccg gct att ggc tac tgg gct cag aac gcg 23
25

Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala Gln Asn Ala

645

650

655

aac ttc cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct 23
73

Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala

660

665

670

675

aaa tct cct gag gca atc gat gcg gtt atc cga aac acc atg att cag 24
21

Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln

680

685

690

ggc atc ttg tcc atc ctg ttc gcg gtg ctc gtc ctc gtt gtt gtc ggc 24
69

Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Val Gly

695

700

705

gca gcc att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga 25
17

Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly

710

715

720

aca cct ttg gag acc act gaa gag cct gat act gaa tct gag ttc ttc 25
65

Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe

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725

730

735

gcc cca act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc 26
13

Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala

740

745

750

755

atg tgg gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg 26
61

Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly

760

765

770

cac taaaacatga tggctcttac tcatgcactg tggaaaatcc cgcgggcggt 27
14

His

gtggtggtat ctactgagc tcatggggga cacggcgtat tccaagtatg tgggtgcactt 27
74

aaagcaccac catccggatg ctccgattcc tactgagcgg gagtattggc gggcaaagta 28
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Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala
20 25 30

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Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile
210 215 220

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Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
325 330 335

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
 420 425 430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
 435 440 445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
 450 455 460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
 465 470 475 480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
 485 490 495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
 500 505 510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
 515 520 525

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
 530 535 540

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
 545 550 555 560

Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
 565 570 575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
 580 585 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
 595 600 605

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Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
625 630 635 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
675 680 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
705 710 715 720

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
740 745 750

Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser
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Ser Gly Gly His
770

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032301.195.seq.ST25.txt

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<212> DNA

<213> *Corynebacterium glutamicum*

<400> 7

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20